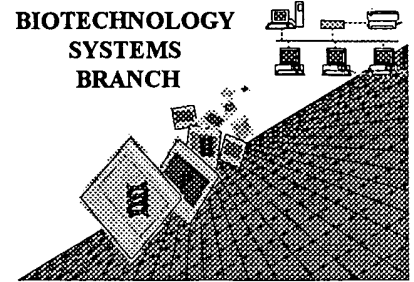


# **RAW SEQUENCE LISTING**

## **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/198,723

Art Unit / Team No. :

0186

Date Processed by STIC:

12/09/98

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:27

INPUT SET: S30248.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

1  
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35  
36  
37  
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45

(1) General Information:

(i) APPLICANT: Malcolm, Bruce  
Taremi, Shahriar S.  
Weber, Patricia  
Yao, Nanhua

(ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus  
NS3 Protease and NS4A Cofactor Peptide

(iii) NUMBER OF SEQUENCES: 123 / 125

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Schering-Plough Corp.  
(B) STREET: 2000 Galloping Hill Road  
(C) CITY: Kenilworth  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07030

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Power Macintosh  
(C) OPERATING SYSTEM: 8.0.1  
(D) SOFTWARE: Microsoft Word 6.0.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McLaughlin, Jaye P.  
(B) REGISTRATION NUMBER: 41,211  
(C) REFERENCE/DOCKET NUMBER: JB0800P2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908)298-5056  
(B) TELEFAX: (908)298-5388

--> OK

--> OK

09/198,723

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Ala Gly Gly  
1

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1964 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..1964

(2) INFORMATION FOR SEQ ID NO:23:

Please Note:

Remove all

format markers  
throughout  
listing. They  
start appearing in  
sequence 1.

← What is this?

(Seq. 22 is  
already mentioned  
above)

9/198,723

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna *delete-enclosed sequence for an open  
and sequence*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr
1				5					10				15		

09/198,723

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS: 646

(A) LENGTH: 668 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	1		5		10		15
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Lys		20		25		30	
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val		35		40		45	
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn		50		55		60	
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala		65		70		75	
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp			85		90		95
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys		100		105		110	
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val		115		120		125	
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro		130		135		140	
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys		145		150		155	
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg			165		170		175
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr		180		185		190	
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val		195		200		205	
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly		210		215		220	
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val		225		230		235	
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr							

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245

250

255

Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg
			260					265					270		
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe
		275					280					285			
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys
	290					295					300				
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr
305					310					315					320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala
				325					330					335	
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu
			340					345					350		
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala
		355					360					365			
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His
	370					375					380				
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly
385					390					395					400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro
				405					410					415	
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly
			420					425					430		
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr
		435					440					445			
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr
	450					455					460				
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr
465					470					475					480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg
				485					490					495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala
			500					505					510		
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu
		515					520					525			
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu
	530					535					540				
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His

*See  
next  
page*

545		550		555		560									
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val
				565					570					575	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser
			580					585					590		
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His
		595					600					605			
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val
	610					615					620				
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala
625					630					635					640
Asp	Leu	Glu	Val	Val	Thr										
			645												
Gly	Arg	Thr	Arg	Ala	Pro	Pro	Pro	Pro	Pro	Leu	Arg				
10			660		15			665		20					

*delete stop codons*  
*Thru via new SEQ ID NO.*  
*1 650 5 655*

Any group of 4 or  
 more amino acids  
 following a stop codon  
 (\*) needs its own  
 SEQ ID NO. Please  
 adjust the  
 (iii) NUMBER OF SEQUENCES,  
 response, too  
 (p. 1)

01/198,723  
(i) SEQUENCE CHARACTERISTICS: → 646 shown

(A) LENGTH: ~~668~~ amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	His	Met	His	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1				5						10					15		
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile		
			20					25					30				
Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val		
		35					40					45					
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn		
	50					55					60						
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala		
65					70					75					80		
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp		
				85					90					95			
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys		
		100						105					110				
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val		
		115					120					125					
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro		
	130					135					140						
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys		
145					150					155					160		
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg		
			165						170					175			
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr		
		180						185					190				
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val		
		195					200					205					
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly		
	210					215					220						
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val		
225					230					235					240		
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr		
			245						250					255			



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Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	260	265	270	
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	275	280	285	
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	290	295	300	
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	305	310	315	320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	325	330	335	
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	340	345	350	
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	355	360	365	
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	370	375	380	
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	385	390	395	400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	405	410	415	
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	420	425	430	
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	435	440	445	
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	450	455	460	
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	465	470	475	480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	485	490	495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	500	505	510	
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	515	520	525	
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	530	535	540	
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	545	550	555	560

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Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val  
565 570 575

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
580 585 590

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His  
595 600 605

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val  
610 615 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
625 630 635 640

Asp Leu Glu Val Val Thr  
645

*\* delete*

↑  
*insert*

09/198,723

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

646 shown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1				5					10					15		
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	
			20					25					30			
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	
		35					40					45				
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
	50					55					60					
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
65					70					75					80	
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
				85					90					95		
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
		100						105					110			
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
		115					120					125				
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135					140					
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	
145					150					155					160	
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230					235					240	
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	

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245

250

255

Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg
			260					265					270		
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe
		275					280					285			
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys
	290					295					300				
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr
305					310					315					320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala
				325					330					335	
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu
			340					345					350		
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala
		355					360					365			
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His
	370					375					380				
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly
385					390					395					400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro
				405					410					415	
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly
			420					425					430		
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr
		435					440					445			
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr
	450					455					460				
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr
465					470					475					480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg
				485					490					495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala
			500					505					510		
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu
		515					520					525			
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu
	530					535					540				
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His



09/198,723

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS: *646 shown*

- (A) LENGTH: ~~668~~ amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	His	Met	His	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala
1				5						10					15	
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	
			20					25					30			
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	
		35					40					45				
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
	50					55					60					
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
65					70					75					80	
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
				85					90					95		
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
		100						105					110			
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
		115					120					125				
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135					140					
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	
145					150					155					160	
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
	195						200					205				
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230					235					240	
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	

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245

250

255

Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg
			260					265					270		
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe
		275					280					285			
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys
	290					295					300				
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr
305					310					315					320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala
				325					330					335	
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu
			340					345					350		
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala
		355					360					365			
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His
	370					375					380				
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly
385					390					395					400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro
				405					410					415	
Thr	Ser	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly
			420					425					430		
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr
		435					440					445			
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr
	450					455					460				
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr
465					470					475					480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg
				485					490					495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala
			500					505					510		
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu
		515					520					525			
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu
	530					535					540				
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His

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245

250

255

Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg
			260					265					270		
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe
		275					280					285			
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys
	290					295					300				
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr
305					310					315					320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala
				325					330					335	
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu
			340					345					350		
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala
		355					360					365			
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His
	370					375					380				
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly
385					390					395					400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro
				405					410					415	
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly
			420					425					430		
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr
		435					440					445			
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr
	450					455					460				
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr
465					470					475					480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg
				485					490					495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala
			500					505					510		
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu
		515					520					525			
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu
	530					535					540				
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His



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545		550		555		560									
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val
			565					570						575	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser
			580					585					590		
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His
		595					600					605			
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val
	610					615					620				
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala
625					630					635					640
Asp	Leu	Glu	Val	Val	Thr										
			645												
Gly	Arg	Thr	Arg	Ala	Pro	Pro	Pro	Pro	Pro	Leu	Arg				
10			660		15			665		20					

(\*) new SEQ ID NO, 1 650 8 655

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 85 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*grou*

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(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:


- (A) LENGTH: 669 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

646 stems

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	1	5	10	15
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	20	25	30	
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	35	40	45	
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	50	55	60	
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	65	70	75	80
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	85	90	95	
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	100	105	110	
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	115	120	125	
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	130	135	140	
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	145	150	155	160
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	165	170	175	
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	180	185	190	
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	195	200	205	
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	210	215	220	
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	225	230	235	240
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr				

545					550					555					560
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val
				565					570					575	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser
			580					585					590		
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His
		595					600					605			
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val
	610					615					620				
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala
625					630					635					640
Asp	Leu	Glu	Val	Val	Thr										
				645											
				↑											

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:35

INPUT SET: S30248.raw

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4176 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT 528
4177 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
4178 165 170 175
4179
4180 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576
4181 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4182 180 185 190
4183
4184 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624
4185 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4186 195 200 205
4187
4188 TCC ATG GAA ACT ACT ATG CGG TCT TGA 651
4189 Ser Met Glu Thr Thr Met Arg Ser *
4190 210 215
4191
4192 (i) SEQUENCE CHARACTERISTICS:
4193 (A) LENGTH: 651 base pairs
4194 (B) TYPE: nucleic acid
4195 (C) STRANDEDNESS: single
4196 (D) TOPOLOGY: linear
4197
4198 (ii) MOLECULE TYPE: DNA (genomic)
4199
4200
4201
4202 (ix) FEATURE:
4203 (A) NAME/KEY: CDS
4204 (B) LOCATION: 1..651
4205
4206
--> 4207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
4208
4209 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48
4210 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
4211 1 5 10 15
4212
4213 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96
4214 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
4215 20 25 30
4216
4217 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144
4218 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
4219 35 40 45
4220
4221 CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192
4222 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
4223 50 55 60
4224
4225 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240
4226 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
4227 65 70 75 80
4228

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*insert a hard return*  
(2) INFORMATION FOR SEQ ID NO:93:

*(delete all  
format markers)  
(e.g., hard page break  
codes)*

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:36

INPUT SET: S30248.raw

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4229 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA      288
4230 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
4231                               85                               90                               95
4232
4233 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT      336
4234 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
4235                               100                               105                               110
4236
4237 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC      384
4238 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
4239                               115                               120                               125
4240
4241 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA      432
4242 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
4243                               130                               135                               140
4244
4245 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4246 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4247                               145                               150                               155                               160
4248
4249 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT      528
4250 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
4251                               165                               170                               175
4252
4253 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4254 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4255                               180                               185                               190
4256
4257 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624
4258 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4259                               195                               200                               205
4260
4261 TCC ATG GAA ACT ACT ATG CGG TCT TGA * hard return      651
4262 Ser Met Glu Thr Thr Met Arg Ser *
4263                               210                               215
4264
4265 (i) SEQUENCE CHARACTERISTICS:
4266 (A) LENGTH: 651 base pairs
4267 (B) TYPE: nucleic acid
4268 (C) STRANDEDNESS: single
4269 (D) TOPOLOGY: linear
4270
4271 (ii) MOLECULE TYPE: DNA (genomic)
4272
4273
4274 (ix) FEATURE:
4275 (A) NAME/KEY: CDS
4276 (B) LOCATION: 1..651
4277
4278
--> 4279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
4280
4281 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:37

INPUT SET: S30248.raw

4282	Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
4283	1 5 10 15	
4284		
4285	CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
4286	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
4287	20 25 30	
4288		
4289	TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
4290	Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
4291	35 40 45	
4292		
4293	CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
4294	Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
4295	50 55 60	
4296		
4297	GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
4298	Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
4299	65 70 75 80	
4300		
4301	ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
4302	Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
4303	85 90 95	
4304		
4305	AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
4306	Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
4307	100 105 110	
4308		
4309	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
4310	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
4311	115 120 125	
4312		
4313	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
4314	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
4315	130 135 140	
4316		
4317	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
4318	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
4319	145 150 155 160	
4320		
4321	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
4322	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
4323	165 170 175	
4324		
4325	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
4326	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
4327	180 185 190	
4328		
4329	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
4330	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
4331	195 200 205	
4332		
4333	TCC ATG GAA ACT ACT ATG CGG TCT TGA	651
4334	Ser Met Glu Thr Thr Met Arg Ser *	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:38

INPUT SET: S30248.raw

210 215 (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 651 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..651

--> (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

4335	ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
4336	Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
4337	1 5 10 15	
4338	CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
4339	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
4340	20 25 30	
4341	TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
4342	Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
4343	35 40 45	
4344	CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
4345	Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
4346	50 55 60	
4347	GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
4348	Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
4349	65 70 75 80	
4350	ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
4351	Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
4352	85 90 95	
4353	AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
4354	Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
4355	100 105 110	
4356	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
4357	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
4358	115 120 125	
4359	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
4360	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
4361	130 135 140	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:38

INPUT SET: S30248.raw

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4388
4389 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4390 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4391 145                      150                      155                      160
4392
4393 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT      528
4394 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
4395                      165                      170                      175
4396
4397 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4398 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4399                      180                      185                      190
4400
4401 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624
4402 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4403                      195                      200                      205
4404
4405 TCC ATG GAA ACT ACT ATG CGG TCT TGA      651
4406 Ser Met Glu Thr Thr Met Arg Ser *
4407 210                      215
4408
4409 (i) SEQUENCE CHARACTERISTICS:
4410 (A) LENGTH: 650 base pairs
4411 (B) TYPE: nucleic acid
4412 (C) STRANDEDNESS: single
4413 (D) TOPOLOGY: linear
4414
4415 (ii) MOLECULE TYPE: cDNA
4416
4417
4418
4419 (ix) FEATURE:
4420 (A) NAME/KEY: CDS
4421 (B) LOCATION: 1..650
4422
4423
--> 4424 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
4425
4426 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
4427 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
4428 1                      5                      10                      15
4429
4430 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
4431 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
4432                      20                      25                      30
4433
4434 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA      144
4435 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
4436                      35                      40                      45
4437
4438 CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC      192
4439 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
4440                      50                      55                      60

```



# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:39

INPUT SET: S30248.raw

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4441
4442 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG      240
4443 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
4444 65                               70                               75                               80
4445
4446 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA      288
4447 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
4448                               85                               90                               95
4449
4450 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT      336
4451 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
4452                               100                               105                               110
4453
4454 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC      384
4455 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
4456                               115                               120                               125
4457
4458 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA      432
4459 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
4460                               130                               135                               140
4461
4462 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4463 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4464 145                               150                               155                               160
4465
4466 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT      528
4467 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
4468                               165                               170                               175
4469
4470 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4471 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4472                               180                               185                               190
4473
4474 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624
4475 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4476                               195                               200                               205
4477
4478 TCC ATG GAA ACT ACT ATG CGG TCT TG      650
4479 Ser Met Glu Thr Thr Met Arg Ser
4480 210                               215

```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..650

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:40

INPUT SET: S30248.raw

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4494
4495
--> 4496      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
4497
4498      ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
4499      Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
4500      1          5          10          15
4501
4502      CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
4503      Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
4504      20          25          30
4505
4506      TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA      144
4507      Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
4508      35          40          45
4509
4510      CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC      192
4511      Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
4512      50          55          60
4513
4514      GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG      240
4515      Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
4516      65          70          75          80
4517
4518      ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA      288
4519      Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
4520      85          90          95
4521
4522      AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT      336
4523      Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
4524      100          105          110
4525
4526      GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC      384
4527      Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
4528      115          120          125
4529
4530      TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA      432
4531      Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
4532      130          135          140
4533
4534      CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4535      His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4536      145          150          155          160
4537
4538      CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT      528
4539      Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
4540      165          170          175
4541
4542      CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4543      Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4544      180          185          190
4545
4546      GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

 DATE: 12/09/98  
 TIME: 16:06:40

INPUT SET: S30248.raw

4547 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 4548 195 200 205  
 4549  
 4550 TCC ATG GAA ACT ACT ATG CGG TCT TG 650  
 4551 Ser Met Glu Thr Thr Met Arg Ser  
 4552 210 215  
 4553  
 4554 (i) SEQUENCE CHARACTERISTICS:  
 4555 (A) LENGTH: 651 base pairs  
 4556 (B) TYPE: nucleic acid  
 4557 (C) STRANDEDNESS: single  
 4558 (D) TOPOLOGY: linear  
 4559  
 4560 (ii) MOLECULE TYPE: cDNA  
 4561  
 4562  
 4563 (ix) FEATURE:  
 4564 (A) NAME/KEY: CDS  
 4565 (B) LOCATION: 1..651  
 4566  
 4567  
 --> 4568 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:  
 4569  
 4570 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
 4571 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 4572 1 5 10 15  
 4573  
 4574 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
 4575 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 4576 20 25 30  
 4577  
 4578 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
 4579 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 4580 35 40 45  
 4581  
 4582 CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
 4583 Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 4584 50 55 60  
 4585  
 4586 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
 4587 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 4588 65 70 75 80  
 4589  
 4590 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
 4591 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 4592 85 90 95  
 4593  
 4594 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
 4595 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 4596 100 105 110  
 4597  
 4598 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384  
 4599 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:41

INPUT SET: S30248.raw

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4600          115          120          125
4601
4602   TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA      432
4603   Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
4604       130          135          140
4605
4606   CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4607   His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4608   145          150          155          160
4609
4610   CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT      528
4611   Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
4612       165          170          175
4613
4614   CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4615   Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4616       180          185          190
4617
4618   GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624
4619   Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4620       195          200          205
4621
4622   TCC ATG GAA ACT ACT ATG CGG TCT TGA      651
4623   Ser Met Glu Thr Thr Met Arg Ser *
4624       210          215
4625   (2) INFORMATION FOR SEQ ID NO:99:
4626   (i) SEQUENCE CHARACTERISTICS:
4627       (A) LENGTH: 651 base pairs
4628       (B) TYPE: nucleic acid
4629       (C) STRANDEDNESS: single
4630       (D) TOPOLOGY: linear
4631
4632   (ii) MOLECULE TYPE: cDNA
4633
4634
4635   (ix) FEATURE:
4636       (A) NAME/KEY: CDS
4637       (B) LOCATION: 1..651
4638
4639
--> 4640   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
4641
4642   ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
4643   Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
4644       1          5          10          15
4645
4646   CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
4647   Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
4648       20          25          30
4649
4650   TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA      144
4651   Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
4652       35          40          45

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:42

INPUT SET: S30248.raw

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4653
4654   CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC      192
4655   Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
4656       50                      55                      60
4657
4658   GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG      240
4659   Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
4660       65                      70                      75                      80
4661
4662   ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA      288
4663   Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
4664       85                      90                      95
4665
4666   AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT      336
4667   Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
4668       100                     105                     110
4669
4670   GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC      384
4671   Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
4672       115                     120                     125
4673
4674   TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA      432
4675   Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
4676       130                     135                     140
4677
4678   CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC      480
4679   His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
4680       145                     150                     155                     160
4681
4682   CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT      528
4683   Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
4684       165                     170                     175
4685
4686   CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC      576
4687   Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
4688       180                     185                     190
4689
4690   GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG      624
4691   Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
4692       195                     200                     205
4693
4694   TCC ATG GAA ACT ACT ATG CGG TCT TGA      651
4695   Ser Met Glu Thr Thr Met Arg Ser *
4696       210                     215

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(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:42

INPUT SET: S30248.raw

4706  
4707 (ix) FEATURE:  
4708 (A) NAME/KEY: CDS  
4709 (B) LOCATION: 1..651  
--> 4710 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
4711  
4712 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
4713 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
4714 1 5 10 15  
4715  
4716 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
4717 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
4718 20 25 30  
4719  
4720 TCT CCT GCT GGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
4721 Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
4722 35 40 45  
4723  
4724 CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
4725 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
4726 50 55 60  
4727  
4728 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
4729 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
4730 65 70 75 80  
4731  
4732 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
4733 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
4734 85 90 95  
4735  
4736 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
4737 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
4738 100 105 110  
4739  
4740 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384  
4741 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
4742 115 120 125  
4743  
4744 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA 432  
4745 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
4746 130 135 140  
4747  
4748 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC 480  
4749 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
4750 145 150 155 160  
4751  
4752 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT 528  
4753 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
4754 165 170 175  
4755  
4756 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576  
4757 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
4758 180 185 190

*100 (use numeral 0, not upper-case O)*

**INPUT SET: S30248.raw**[illegible]

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:47

INPUT SET: S30248.raw

5023 Cys Met Ser Ala Asp Leu Glu Val Val  
5024 660 665

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1997

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

5044 --> ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
5045
5046 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
5047 1 5 10 15
5048
5049 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
5050 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
5051 20 25 30
5052
5053 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA      144
5054 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
5055 35 40 45
5056
5057 CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC      192
5058 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
5059 50 55 60
5060
5061 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG      240
5062 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
5063 65 70 75 80
5064
5065 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA      288
5066 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
5067 85 90 95
5068
5069 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT      336
5070 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
5071 100 105 110
5072
5073 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC      384
5074 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
5075

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:48

INPUT SET: S30248.raw

5076	115	120	125	
5077				
5078	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432		
5079	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg			
5080	130	135	140	
5081				
5082	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480		
5083	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser			
5084	145	150	155	160
5085				
5086	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528		
5087	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly			
5088		165	170	175
5089				
5090	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576		
5091	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala			
5092		180	185	190
5093				
5094	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624		
5095	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu			
5096		195	200	205
5097				
5098	TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672		
5099	Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser			
5100		210	215	220
5101				
5102	CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC	720		
5103	Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro			
5104		225	230	235
5105				
5106	ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA	768		
5107	Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln			
5108		245	250	255
5109				
5110	GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG	816		
5111	Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly			
5112		260	265	270
5113				
5114	TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA	864		
5115	Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg			
5116		275	280	285
5117				
5118	ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC	912		
5119	Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr			
5120		290	295	300
5121				
5122	TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC	960		
5123	Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp			
5124		305	310	315
5125				
5126	ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG	1008		
5127	Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu			
5128		325	330	335

**INPUT SET: S30248.raw**

5129																		
5130	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT		1056
5131	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu		
5132				340					345					350				
5133																		
5134	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC		1104
5135	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His		
5136			355					360					365					
5137																		
5138	CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC		1152
5139	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe		
5140		370					375					380						
5141																		
5142	TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC		1200
5143	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu		
5144	385					390					395					400		
5145																		
5146	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG		1248
5147	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu		
5148				405					410						415			
5149																		
5150	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG		1296
5151	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val		
5152			420					425					430					
5153																		
5154	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT		1344
5155	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala		
5156			435				440						445					
5157																		
5158	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC		1392
5159	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn		
5160		450					455					460						
5161																		
5162	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC		1440
5163	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr		
5164	465					470					475					480		
5165																		
5166	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG							

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

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INPUT SET: S30248.raw

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5182   TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC      1680
5183   Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
5184   545                               550                               555                               560
5185
5186   CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT      1728
5187   Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
5188                               565                               570                               575
5189
5190   ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC      1776
5191   Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
5192                               580                               585                               590
5193
5194   CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC      1824
5195   Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
5196   595                               600                               605
5197
5198   CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA      1872
5199   Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
5200   610                               615                               620
5201
5202   CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC      1920
5203   Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
5204   625                               630                               635                               640
5205
5206   CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA      1968
5207   Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
5208                               645                               650                               655
5209
5210   TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT      1998
5211   Cys Met Ser Ala Asp Leu Glu Val Val
5212   660                               665
5213
5214       (i) SEQUENCE CHARACTERISTICS:
5215           (A) LENGTH: 1998 base pairs
5216           (B) TYPE: nucleic acid
5217           (C) STRANDEDNESS: single
5218           (D) TOPOLOGY: linear
5219
5220       (ii) MOLECULE TYPE: cDNA
5221
5222
5223
5224
5225       (ix) FEATURE:
5226           (A) NAME/KEY: CDS
5227           (B) LOCATION: 1..1995
5228
5229
5230       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
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5232   ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
5233   Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
5234   1                               5                               10                               15

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**INPUT SET: S30248.raw**

5235																		
5236	CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA		96
5237	Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu		
5238				20														
5239																		
5240	TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA		144
5241	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu		
5242			35					40					45					
5243																		
5244	CTT	GGT	TGC	ATC	AAG	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC		192
5245	Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val		
5246		50					55					60						
5247																		
5248	GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG		240
5249	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala		
5250	65					70				75						80		
5251																		
5252	ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA		288
5253	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser		
5254					85					90					95			
5255																		
5256	AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT		336
5257	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn		
5258				100					105					110				
5259																		
5260	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC		384
5261	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser		
5262			115					120					125					
5263																		
5264	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA		432
5265	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg		
5266		130					135					140						
5267																		
5268	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC		480
5269	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser		
5270	145					150					155					160		
5271																		
5272	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT		

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

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5288	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
5289	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
5290	225					230					235					240	
5291																	
5292	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
5293	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
5294					245					250					255		
5295																	
5296	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
5297	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
5298					260				265					270			
5299																	
5300	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
5301	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
5302			275					280					285				
5303																	
5304	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
5305	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
5306			290					295				300					
5307																	
5308	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
5309	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
5310	305					310					315					320	
5311																	
5312	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
5313	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
5314					325					330					335		
5315																	
5316	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
5317	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
5318					340				345				350				
5319																	
5320	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
5321	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
5322			355					360				365					
5323																	
5324	CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
5325	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
5326			370				375					380					
5327																	
5328	TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
5329	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
5330	385					390					395					400	
5331																	
5332	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
5333	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
5334					405				410					415			
5335																	
5336	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
5337	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
5338					420				425					430			
5339																	
5340	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

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*INPUT SET: S30248.raw*

5341	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
5342			435					440					445				
5343																	
5344	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
5345	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
5346		450					455					460					
5347																	
5348	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
5349	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
5350	465					470					475					480	
5351																	
5352	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
5353	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
5354					485				490						495		
5355																	
5356	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
5357	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
5358				500				505						510			
5359																	
5360	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
5361	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
5362			515					520					525				
5363																	
5364	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	1632
5365	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
5366		530					535					540					
5367																	
5368	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
5369	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
5370	545					550					555					560	
5371																	
5372	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
5373	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
5374					565				570						575		
5375																	
5376	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
5377	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
5378				580				585						590			
5379																	
5380	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	1824
5381	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	
5382			595					600					605				
5383																	
5384	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	1872
5385	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	
5386		610					615					620					
5387																	
5388	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	1920
5389	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	
5390	625					630					635					640	
5391																	
5392	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	1968
5393	Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

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5394 645 650 655  
 5395  
 5396 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
 5397 Cys Met Ser Ala Asp Leu Glu Val Val  
 5398 660 665 (2) INFORMATION FOR SEQ ID NO:105:  
 5399  
 5400 (i) SEQUENCE CHARACTERISTICS:  
 5401 (A) LENGTH: 1998 base pairs  
 5402 (B) TYPE: nucleic acid  
 5403 (C) STRANDEDNESS: single  
 5404 (D) TOPOLOGY: linear  
 5405  
 5406 (ii) MOLECULE TYPE: cDNA  
 5407  
 5408  
 5409  
 5410 (ix) FEATURE:  
 5411 (A) NAME/KEY: CDS  
 5412 (B) LOCATION: 1..1995  
 5413  
 5414  
 --> 5415 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:  
 5416  
 5417 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
 5418 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 5419 1 5 10 15  
 5420  
 5421 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
 5422 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 5423 20 25 30  
 5424  
 5425 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
 5426 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 5427 35 40 45  
 5428  
 5429 CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
 5430 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 5431 50 55 60  
 5432  
 5433 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
 5434 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 5435 65 70 75 80  
 5436  
 5437 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
 5438 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 5439 85 90 95  
 5440  
 5441 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
 5442 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 5443 100 105 110  
 5444  
 5445 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384  
 5446 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

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INPUT SET: S30248.raw

5447		115		120		125													
5448																			
5449	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA		432	
5450	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg			
5451		130					135					140							
5452																			
5453	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC		480	
5454	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser			
5455	145					150					155					160			
5456																			
5457	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT		528	
5458	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly			
5459					165					170					175				
5460																			
5461	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC		576	
5462	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala			
5463				180				185					190						
5464																			
5465	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG		624	
5466	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu			
5467			195				200					205							
5468																			
5469	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC		672	
5470	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser			
5471		210					215					220							
5472																			
5473	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC		720	
5474	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro			
5475	225					230					235					240			
5476																			
5477	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA		768	
5478	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln			
5479					245				250						255				
5480																			
5481	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG		816	
5482	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly			
5483				260				265						270					
5484																			
5485	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA		864	
5486	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg			
5487			275				280					285							
5488																			
5489	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC		912	
5490	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr			
5491		290					295					300							
5492																			
5493	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC		960	
5494	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp			
5495	305					310				315						320			
5496																			
5497	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG		1008	
5498	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu			
5499					325				330						335				



**INPUT SET: S30248.raw**

5500																		
5501	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT		1056
5502	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu		
5503				340					345					350				
5504																		
5505	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC		1104
5506	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His		
5507			355					360					365					
5508																		
5509	CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC		1152
5510	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe		
5511		370					375					380						
5512																		
5513	TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC		1200
5514	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu		
5515	385					390					395					400		
5516																		
5517	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG		1248
5518	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu		
5519				405					410						415			
5520																		
5521	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG		1296
5522	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val		
5523			420					425					430					
5524																		
5525	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT		1344
5526	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala		
5527			435				440						445					
5528																		
5529	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC		1392
5530	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn		
5531		450					455					460						
5532																		
5533	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC		1440
5534	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr		
5535	465				470					475						480		
5536																		
5537	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG		1488</

**INPUT SET: S30248.raw**

	TCG	GTT	AGG	TGG	CGC	TAC	CAT	AAC	ACA	CCA	TTG	CCC	GTT	TGC		1680	
5554	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
5555	545					550				555					560		
5556																	
5557	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
5558	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
5559					565				570					575			
5560																	
5561	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
5562	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
5563				580				585					590				
5564																	
5565	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	1824
5566	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	
5567			595				600					605					
5568																	
5569	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	1872
5570	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	
5571		610					615					620					
5572																	
5573	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	1920
5574	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	
5575	625					630					635				640		
5576																	
5577	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	1968
5578	Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	
5579					645				650					655			
5580																	
5581	TGC	ATG	TCG	GCT	GAC	CTG	GAG	GTC	GTC	ACT							1998
5582	Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Val								
5583				660					665								
5584																	
5585	(i)	SEQUENCE CHARACTERISTICS:															
5586		(A) LENGTH: 1998 base pairs															
5587		(B) TYPE: nucleic acid															
5588		(C) STRANDEDNESS: single															
5589		(D) TOPOLOGY: linear															
5590																	
5591	(ii)	MOLECULE TYPE:															

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:54

INPUT SET: S30248.raw

5606	CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
5607	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
5608	20 25 30	
5609		
5610	TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
5611	Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
5612	35 40 45	
5613		
5614	CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
5615	Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
5616	50 55 60	
5617		
5618	GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
5619	Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
5620	65 70 75 80	
5621		
5622	ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
5623	Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
5624	85 90 95	
5625		
5626	AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
5627	Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
5628	100 105 110	
5629		
5630	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
5631	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
5632	115 120 125	
5633		
5634	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
5635	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
5636	130 135 140	
5637		
5638	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
5639	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
5640	145 150 155 160	
5641		
5642	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
5643	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
5644	165 170 175	
5645		
5646	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
5647	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
5648	180 185 190	
5649		
5650	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
5651	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
5652	195 200 205	
5653		
5654	TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
5655	Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	
5656	210 215 220	
5657		
5658	CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC	720

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

DATE: 12/09/98  
TIME: 16:06:55

INPUT SET: S30248.raw

5659	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
5660	225					230					235					240	
5661																	
5662	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
5663	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
5664					245					250						255	
5665																	
5666	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
5667	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
5668				260					265						270		
5669																	
5670	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
5671	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
5672			275					280					285				
5673																	
5674	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
5675	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
5676			290				295					300					
5677																	
5678	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
5679	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
5680	305					310					315					320	
5681																	
5682	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
5683	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
5684				325						330					335		
5685																	
5686	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
5687	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
5688				340					345					350			
5689																	
5690	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
5691	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
5692			355					360					365				
5693																	
5694	CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
5695	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
5696		370					375					380					
5697																	
5698	TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
5699	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
5700	385					390					395					400	
5701																	
5702	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
5703	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
5704					405					410					415		
5705																	
5706	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
5707	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
5708				420					425					430			
5709																	
5710	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
5711	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
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INPUT SET: S30248.raw

5712		435		440		445												
5713																		
5714	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC		1392
5715	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn		
5716		450					455					460						
5717																		
5718	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC		1440
5719	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr		
5720	465					470					475					480		
5721																		
5722	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG		1488
5723	Ile	Glu	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg			
5724				485				490						495				
5725																		
5726	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT		1536
5727	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr		
5728				500				505						510				
5729																		
5730	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG		1584
5731	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu		
5732			515					520					525					
5733																		
5734	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC		1632
5735	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr		
5736		530					535				540							
5737																		
5738	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC		1680
5739	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys		
5740	545					550				555						560		
5741																		
5742	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT		1728
5743	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His		
5744				565				570						575				
5745																		
5746	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC		1776
5747	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe		
5748			580					585					590					
5749																		
5750	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC		1824
5751	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala		
5752			595					600					605					
5753																		
5754	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA		1872
5755	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys		
5756		610					615					620						
5757																		
5758	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC		1920
5759	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val		
5760	625					630					635					640		
5761																		
5762	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA		1968
5763	Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala		
5764				645					650						655			

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:57

INPUT SET: S30248.raw

5765  
5766 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
5767 Cys Met Ser Ala Asp Leu Glu Val Val  
5768 660 665 (2) INFORMATION FOR SEQ ID NO:107:  
5769  
5770 (i) SEQUENCE CHARACTERISTICS:  
5771 (A) LENGTH: 1998 base pairs  
5772 (B) TYPE: nucleic acid  
5773 (C) STRANDEDNESS: single  
5774 (D) TOPOLOGY: linear  
5775  
5776 (ii) MOLECULE TYPE: cDNA  
5777  
5778  
5779 (ix) FEATURE:  
5780 (A) NAME/KEY: CDS  
5781 (B) LOCATION: 1..1997  
5782  
5783 (ix) FEATURE:  
5784 (A) NAME/KEY: CDS  
5785 (B) LOCATION: 1..1995  
5786  
5787  
--> 5788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:  
5789  
5790 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
5791 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
5792 1 5 10 15  
5793  
5794 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
5795 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
5796 20 25 30  
5797  
5798 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
5799 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
5800 35 40 45  
5801  
5802 CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
5803 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
5804 50 55 60  
5805  
5806 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
5807 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
5808 65 70 75 80  
5809  
5810 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
5811 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
5812 85 90 95  
5813  
5814 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
5815 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
5816 100 105 110  
5817

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:58

INPUT SET: S30248.raw

5818	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
5819	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
5820	115 120 125	
5821		
5822	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
5823	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
5824	130 135 140	
5825		
5826	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
5827	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
5828	145 150 155 160	
5829		
5830	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
5831	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
5832	165 170 175	
5833		
5834	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
5835	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
5836	180 185 190	
5837		
5838	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
5839	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
5840	195 200 205	
5841		
5842	TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
5843	Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	
5844	210 215 220	
5845		
5846	CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC	720
5847	Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro	
5848	225 230 235 240	
5849		
5850	ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA	768
5851	Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln	
5852	245 250 255	
5853		
5854	GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG	816
5855	Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly	
5856	260 265 270	
5857		
5858	TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA	864
5859	Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg	
5860	275 280 285	
5861		
5862	ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC	912
5863	Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr	
5864	290 295 300	
5865		
5866	TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC	960
5867	Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp	
5868	305 310 315 320	
5869		
5870	ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG	1008

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:58

INPUT SET: S30248.raw

5871	Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu	
5872	325 330 335	
5873		
5874	GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT	1056
5875	Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu	
5876	340 345 350	
5877		
5878	GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC	1104
5879	Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His	
5880	355 360 365	
5881		
5882	CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC	1152
5883	Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe	
5884	370 375 380	
5885		
5886	TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC	1200
5887	Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu	
5888	385 390 395 400	
5889		
5890	ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG	1248
5891	Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu	
5892	405 410 415	
5893		
5894	TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG	1296
5895	Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val	
5896	420 425 430	
5897		
5898	TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT	1344
5899	Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala	
5900	435 440 445	
5901		
5902	CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC	1392
5903	Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn	
5904	450 455 460	
5905		
5906	ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC	1440
5907	Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr	
5908	465 470 475 480	
5909		
5910	ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG	1488
5911	Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg	
5912	485 490 495	
5913		
5914	CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT	1536
5915	Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr	
5916	500 505 510	
5917		
5918	CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG	1584
5919	Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu	
5920	515 520 525	
5921		
5922	TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC	1632
5923	Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr	



# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:06:59

INPUT SET: S30248.raw

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5924      530      535      540
5925
5926 TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC      1680
5927 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
5928 545      550      555      560
5929
5930 CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT      1728
5931 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
5932      565      570      575
5933
5934 ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC      1776
5935 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
5936      580      585      590
5937
5938 CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC      1824
5939 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
5940      595      600      605
5941
5942 CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA      1872
5943 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
5944 610      615      620
5945
5946 CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC      1920
5947 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
5948 625      630      635      640
5949
5950 CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA      1968
5951 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
5952      645      650      655
5953
5954 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT      1998
5955 Cys Met Ser Ala Asp Leu Glu Val Val
5956      660      665
5957
5958 (i) SEQUENCE CHARACTERISTICS:
5959 (A) LENGTH: 1998 base pairs
5960 (B) TYPE: nucleic acid
5961 (C) STRANDEDNESS: single
5962 (D) TOPOLOGY: linear
5963
5964 (ii) MOLECULE TYPE: cDNA
5965
5966
5967
5968
5969 (ix) FEATURE:
5970 (A) NAME/KEY: CDS
5971 (B) LOCATION: 1..1995
5972
5973
--> 5974 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108
5975
5976 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:00

INPUT SET: S30248.raw

5977	Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
5978	1 5 10 15	
5979		
5980	CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
5981	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
5982	20 25 30	
5983		
5984	TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
5985	Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
5986	35 40 45	
5987		
5988	CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
5989	Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
5990	50 55 60	
5991		
5992	GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
5993	Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
5994	65 70 75 80	
5995		
5996	ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
5997	Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
5998	85 90 95	
5999		
6000	AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
6001	Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
6002	100 105 110	
6003		
6004	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
6005	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
6006	115 120 125	
6007		
6008	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
6009	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
6010	130 135 140	
6011		
6012	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
6013	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
6014	145 150 155 160	
6015		
6016	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
6017	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
6018	165 170 175	
6019		
6020	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
6021	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
6022	180 185 190	
6023		
6024	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
6025	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
6026	195 200 205	
6027		
6028	TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
6029	Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:00

INPUT SET: S30248.raw

6030	210	215	220	
6031				
6032	CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC			720
6033	Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro			
6034	225	230	235	240
6035				
6036	ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA			768
6037	Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln			
6038		245	250	255
6039				
6040	GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG			816
6041	Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly			
6042		260	265	270
6043				
6044	TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA			864
6045	Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg			
6046		275	280	285
6047				
6048	ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC			912
6049	Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr			
6050		290	295	300
6051				
6052	TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC			960
6053	Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp			
6054	305	310	315	320
6055				
6056	ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG			1008
6057	Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu			
6058		325	330	335
6059				
6060	GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT			1056
6061	Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu			
6062		340	345	350
6063				
6064	GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC			1104
6065	Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His			
6066		355	360	365
6067				
6068	CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC			1152
6069	Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe			
6070		370	375	380
6071				
6072	TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC			1200
6073	Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu			
6074	385	390	395	400
6075				
6076	ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG			1248
6077	Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu			
6078		405	410	415
6079				
6080	TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG			1296
6081	Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val			
6082		420	425	430

**INPUT SET: S30248.raw**

6083																	
6084	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
6085	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
6086			435					440					445				
6087																	
6088	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
6089	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
6090		450					455					460					
6091																	
6092	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
6093	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
6094	465					470					475					480	
6095																	
6096	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
6097	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
6098					485				490						495		
6099																	
6100	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
6101	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
6102				500					505					510			
6103																	
6104	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
6105	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
6106			515					520					525				
6107																	
6108	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	1632
6109	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
6110		530					535					540					
6111																	
6112	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
6113	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
6114	545					550					555					560	
6115																	
6116	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
6117	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
6118					565					570					575		
6119																	
6120	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
6121	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
6122				580					585					590			
6123																	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:02

INPUT SET: S30248.raw

6136 CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA 1968  
6137 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
6138 645 650 655  
6139

6140 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
6141 Cys Met Ser Ala Asp Leu Glu Val Val  
6142 660 665 (2) INFORMATION FOR SEQ ID NO:109:  
6143

6144 (i) SEQUENCE CHARACTERISTICS:  
6145 (A) LENGTH: 1998 base pairs  
6146 (B) TYPE: nucleic acid  
6147 (C) STRANDEDNESS: single  
6148 (D) TOPOLOGY: linear  
6149

6150 (ii) MOLECULE TYPE: cDNA  
6151  
6152

6153 (ix) FEATURE:  
6154 (A) NAME/KEY: CDS  
6155 (B) LOCATION: 1..1997  
6156

6157 (ix) FEATURE:  
6158 (A) NAME/KEY: CDS  
6159 (B) LOCATION: 1..1995  
6160  
6161

--> 6162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

6163  
6164 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
6165 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
6166 1 5 10 15  
6167  
6168 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
6169 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
6170 20 25 30  
6171  
6172 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
6173 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
6174 35 40 45  
6175  
6176 CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
6177 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
6178 50 55 60  
6179  
6180 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
6181 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
6182 65 70 75 80  
6183  
6184 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
6185 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
6186 85 90 95  
6187  
6188 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:02

INPUT SET: S30248.raw

6189	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
6190				100					105							110	
6191																	
6192	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
6193	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
6194			115					120					125				
6195																	
6196	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
6197	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
6198			130				135					140					
6199																	
6200	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
6201	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
6202						150					155					160	
6203																	
6204	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	GCT	GGT	GGT	528
6205	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	
6206					165				170						175		
6207																	
6208	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
6209	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
6210				180					185					190			
6211																	
6212	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
6213	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
6214			195					200					205				
6215																	
6216	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
6217	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
6218			210				215					220					
6219																	
6220	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
6221	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
6222			225			230					235					240	
6223																	
6224	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
6225	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
6226					245				250					255			
6227																	
6228	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
6229	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
6230				260					265					270			
6231																	
6232	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
6233	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
6234			275					280					285				
6235																	
6236	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
6237	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
6238			290				295					300					
6239																	
6240	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
6241	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:03

INPUT SET: S30248.raw

	305	310	315	320	
6242					
6243					
6244	ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG				1008
6245	Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu				
6246		325	330	335	
6247					
6248	GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT				1056
6249	Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu				
6250		340	345	350	
6251					
6252	GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC				1104
6253	Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His				
6254		355	360	365	
6255					
6256	CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC				1152
6257	Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe				
6258		370	375	380	
6259					
6260	TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC				1200
6261	Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu				
6262		385	390	395	400
6263					
6264	ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG				1248
6265	Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu				
6266		405	410	415	
6267					
6268	TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG				1296
6269	Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val				
6270		420	425	430	
6271					
6272	TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT				1344
6273	Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Val Thr Asp Ala				
6274		435	440	445	
6275					
6276	CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC				1392
6277	Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn				
6278		450	455	460	
6279					
6280	ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC				1440
6281	Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr				
6282		465	470	475	480
6283					
6284	ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG				1488
6285	Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg				
6286		485	490	495	
6287					
6288	CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT				1536
6289	Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr				
6290		500	505	510	
6291					
6292	CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG				1584
6293	Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu				
6294		515	520	525	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:04

INPUT SET: S30248.raw

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6295
6296   TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC      1632
6297   Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr
6298       530                               535                               540
6299
6300   TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC      1680
6301   Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys
6302   545                               550                               555                               560
6303
6304   CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT      1728
6305   Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
6306       565                               570                               575
6307
6308   ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC      1776
6309   Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe
6310       580                               585                               590
6311
6312   CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC      1824
6313   Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala
6314       595                               600                               605
6315
6316   CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA      1872
6317   Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys
6318       610                               615                               620
6319
6320   CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC      1920
6321   Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val
6322   625                               630                               635                               640
6323
6324   CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA      1968
6325   Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
6326       645                               650                               655
6327
6328   TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT      1998
6329   Cys Met Ser Ala Asp Leu Glu Val Val
6330       660                               665

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(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2013

-->



# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:04

INPUT SET: S30248.raw

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--> 6348      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
6349
6350      ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
6351      Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
6352      1          5          10          15
6353
6354      CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT      96
6355      Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile
6356      20          25          30
6357
6358      GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC      144
6359      Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser
6360      35          40          45
6361
6362      CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC      192
6363      Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly
6364      50          55          60
6365
6366      CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA      240
6367      Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala
6368      65          70          75          80
6369
6370      ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT      288
6371      Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val
6372      85          90          95
6373
6374      TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC      336
6375      Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile
6376      100          105          110
6377
6378      ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG      384
6379      Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala
6380      115          120          125
6381
6382      CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC      432
6383      Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp
6384      130          135          140
6385
6386      CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG      480
6387      Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg
6388      145          150          155          160
6389
6390      GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG      528
6391      Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu
6392      165          170          175
6393
6394      AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG      576
6395      Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val
6396      180          185          190
6397
6398      GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG      624
6399      Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val
6400      195          200          205
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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/198,723**

DATE: 12/09/98  
TIME: 16:07:05

**INPUT SET: S30248.raw**

6401																		
6402	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC		672
6403	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val		
6404		210					215					220						
6405																		
6406	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG		720
6407	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val		
6408	225					230					235					240		
6409																		
6410	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG		768
6411	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro		
6412					245					250					255			
6413																		
6414	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC		816
6415	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser		
6416				260					265					270				
6417																		
6418	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT		864
6419	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly		
6420			275					280					285					
6421																		
6422	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC		912
6423	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala		
6424		290					295					300						
6425																		
6426	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC		960
6427	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys		
6428	305					310					315					320		
6429																		
6430	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT		1008
6431	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr		
6432				325						330					335			
6433																		
6434	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG		1056
6435	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu		
6436				340					345					350				
6437																		
6438	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA		1104
6439</																		

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:06

INPUT SET: S30248.raw

6454	GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT	1296
6455	Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr	
6456	420 425 430	
6457		
6458	TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT	1344
6459	Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val	
6460	435 440 445	
6461		
6462	GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC	1392
6463	Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp	
6464	450 455 460	
6465		
6466	TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC	1440
6467	Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser	
6468	465 470 475 480	
6469		
6470	TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA	1488
6471	Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala	
6472	485 490 495	
6473		
6474	GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC	1536
6475	Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Gly	
6476	500 505 510	
6477		
6478	ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT	1584
6479	Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp	
6480	515 520 525	
6481		
6482	TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG	1632
6483	Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu	
6484	530 535 540	
6485		
6486	CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA	1680
6487	Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr	
6488	545 550 555 560	
6489		
6490	CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC	1728
6491	Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val	
6492	565 570 575	
6493		
6494	TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG	1776
6495	Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys	
6496	580 585 590	
6497		
6498	CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG	1824
6499	Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val	
6500	595 600 605	
6501		
6502	TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG	1872
6503	Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys	
6504	610 615 620	
6505		
6506	TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG	1920

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

DATE: 12/09/98  
TIME: 16:07:07

INPUT SET: S30248.raw

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6507 Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu
6508 625                      630                      635                      640
6509
6510 TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA      1968
6511 Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile
6512                      645                      650                      655
6513
6514 ACC AAA TAC ATC ATG GCA TGC ATG TCG GCT GAC CTG GAG GTC GTC      2013
6515 Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val
6516                      660                      665                      670
6517
6518 ACT
6519
6520 (i) SEQUENCE CHARACTERISTICS:
--> 6521 (A) LENGTH: 2016 base pairs
6522 (B) TYPE: nucleic acid
6523 (C) STRANDEDNESS: single
6524 (D) TOPOLOGY: linear
6525
6526 (ii) MOLECULE TYPE: cDNA
6527
6528
6529 (ix) FEATURE:
6530 (A) NAME/KEY: CDS
6531 (B) LOCATION: 1..2013
6532
6533
--> 6534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
6535
6536 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
6537 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
6538 1                      5                      10                      15
6539
6540 CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT      96
6541 Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile
6542                      20                      25                      30
6543
6544 GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC      144
6545 Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser
6546                      35                      40                      45
6547
6548 CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC      192
6549 Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly
6550                      50                      55                      60
6551
6552 CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA      240
6553 Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala
6554 65                      70                      75                      80
6555
6556 ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT      288
6557 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val
6558                      85                      90                      95
6559

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2016(2) INFORM

*Handwritten:*  
Hand  
return

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:07

INPUT SET: S30248.raw

6560	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	336
6561	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	
6562				100					105					110			
6563																	
6564	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	384
6565	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	
6566			115					120					125				
6567																	
6568	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	432
6569	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	
6570			130				135					140					
6571																	
6572	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	480
6573	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	
6574	145					150					155					160	
6575																	
6576	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	528
6577	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	
6578					165				170						175		
6579																	
6580	AAG	GGC	TCT	GCT	GGT	GGT	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	576
6581	Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	
6582				180					185					190			
6583																	
6584	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	624
6585	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	
6586			195					200					205				
6587																	
6588	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	672
6589	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	
6590			210				215					220					
6591																	
6592	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	720
6593	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	
6594	225					230					235					240	
6595																	
6596	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	768
6597	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	
6598					245				250						255		
6599																	
6600	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	816
6601	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	
6602				260					265					270			
6603																	
6604	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	864
6605	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	
6606			275					280					285				
6607																	
6608	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	912
6609	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	
6610			290				295					300					
6611																	
6612	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	960

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:08

INPUT SET: S30248.raw

6613	Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
6614	305 310 315 320	
6615		
6616	TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT	1008
6617	Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
6618	325 330 335	
6619		
6620	GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG	1056
6621	Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu	
6622	340 345 350	
6623		
6624	ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA	1104
6625	Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly	
6626	355 360 365	
6627		
6628	TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT	1152
6629	Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn	
6630	370 375 380	
6631		
6632	ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC	1200
6633	Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile	
6634	385 390 395 400	
6635		
6636	AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC	1248
6637	Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp	
6638	405 410 415	
6639		
6640	GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT	1296
6641	Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr	
6642	420 425 430	
6643		
6644	TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT	1344
6645	Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val	
6646	435 440 445	
6647		
6648	GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC	1392
6649	Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp	
6650	450 455 460	
6651		
6652	TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC	1440
6653	Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser	
6654	465 470 475 480	
6655		
6656	TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA	1488
6657	Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala	
6658	485 490 495	
6659		
6660	GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC	1536
6661	Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly	
6662	500 505 510	
6663		
6664	ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT	1584
6665	Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:09

INPUT SET: S30248.raw

6666	515	520	525	
6667				
6668	TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG	1632		
6669	Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu			
6670	530 535 540			
6671				
6672	CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA	1680		
6673	Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr			
6674	545 550 555 560			
6675				
6676	CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC	1728		
6677	Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val			
6678	565 570 575			
6679				
6680	TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG	1776		
6681	Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys			
6682	580 585 590			
6683				
6684	CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG	1824		
6685	Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val			
6686	595 600 605			
6687				
6688	TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG	1872		
6689	Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys			
6690	610 615 620			
6691				
6692	TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG	1920		
6693	Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu			
6694	625 630 635 640			
6695				
6696	TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA	1968		
6697	Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile			
6698	645 650 655			
6699				
6700	ACC AAA TAC ATC ATG GCA TGC ATG TCG GCT GAC CTG GAG GTC GTC	2013		
6701	Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val			
6702	660 665 670			
6703				
6704	ACT	2016(2) INFORM		
6705				
6706	(i) SEQUENCE CHARACTERISTICS:			
6707	(A) LENGTH: 648 base pairs			
6708	(B) TYPE: nucleic acid			
6709	(C) STRANDEDNESS: single			
6710	(D) TOPOLOGY: linear			
6711				
6712	(ii) MOLECULE TYPE: cDNA			
6713				
6714				
6715	(ix) FEATURE:			
6716	(A) NAME/KEY: CDS			
6717	(B) LOCATION: 1..648			
6718				

hand  
return

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:10

INPUT SET: S30248.raw

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6719
--> 6720      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
6721
6722      ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
6723      Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
6724      1          5          10          15
6725
6726      CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
6727      Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
6728      20          25          30
6729
6730      TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT      144
6731      Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
6732      35          40          45
6733
6734      GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG      192
6735      Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
6736      50          55          60
6737
6738      GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC      240
6739      Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
6740      65          70          75          80
6741
6742      TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG      288
6743      Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
6744      85          90          95
6745
6746      ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG      336
6747      Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val
6748      100          105          110
6749
6750      GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG      384
6751      Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu
6752      115          120          125
6753
6754      ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT      432
6755      Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His
6756      130          135          140
6757
6758      GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG      480
6759      Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu
6760      145          150          155          160
6761
6762      CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA      528
6763      Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
6764      165          170          175
6765
6766      CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA      576
6767      Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val
6768      180          185          190
6769
6770      TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC      624
6771      Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:10

INPUT SET: S30248.raw

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6772          195          200          205
6773
6774 ATG GAA ACT ACT ATG CGG TCT TGA
6775 Met Glu Thr Thr Met Arg Ser *
6776      210          215 (2) INFORMATION FOR SEQ ID NO:113:
6777
6778 (i) SEQUENCE CHARACTERISTICS:
6779 (A) LENGTH: 648 base pairs
6780 (B) TYPE: nucleic acid
6781 (C) STRANDEDNESS: single
6782 (D) TOPOLOGY: linear
6783
6784 (ii) MOLECULE TYPE: cDNA
6785
6786
6787 (ix) FEATURE:
6788 (A) NAME/KEY: CDS
6789 (B) LOCATION: 1..640
6790
6791
--> 6792 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113
6793
6794 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48
6795 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
6796      1          5          10          15
6797
6798 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96
6799 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
6800          20          25          30
6801
6802 TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT 144
6803 Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
6804          35          40          45
6805
6806 GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG 192
6807 Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
6808          50          55          60
6809
6810 GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC 240
6811 Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
6812          65          70          75          80
6813
6814 TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG 288
6815 Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
6816          85          90          95
6817
6818 ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG 336
6819 Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val
6820          100          105          110
6821
6822 GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG 384
6823 Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu
6824          115          120          125

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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION** *US/09/198,723*

DATE: 12/09/98  
TIME: 16:07:11

**INPUT SET: S30248.raw**

6825																				
6826	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT				432
6827	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His				
6828		130					135					140								
6829																				
6830	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG				480
6831	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu				
6832	145					150					155					160				
6833																				
6834	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA				528
6835	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro				
6836					165					170					175					
6837																				
6838	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA				576
6839	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val				
6840				180					185					190						
6841																				
6842	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC				624
6843	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser				
6844			195				200						205							
6845																				
6846	ATG	GAA	ACT	ACT	ATG	C	GGTCTTGA													648
6847	Met	Glu	Thr	Thr	Met															
6848		210																		

(2) INFORMATION FOR SEQ ID NO:114:

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

DATE: 12/09/98  
TIME: 16:07:12

INPUT SET: S30248.raw

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6878  GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG      192
6879  Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln
6880      50                      55                      60
6881
6882  GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA      240
6883  Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro
6884      65                      70                      75                      80
6885
6886  TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC      288
6887  Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp
6888      85                      90                      95
6889
6890  GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC      336
6891  Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser
6892      100                      105                      110
6893
6894  CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC      384
6895  Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu
6896      115                      120                      125
6897
6898  TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC      432
6899  Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr
6900      130                      135                      140
6901
6902  CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA      480
6903  Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu
6904      145                      150                      155                      160
6905
6906  ACT ACT ATG CGG TCT TGA      498
6907  Thr Thr Met Arg Ser *
6908      165
6909  (2) INFORMATION FOR SEQ ID NO:115:
6910      (i) SEQUENCE CHARACTERISTICS:
6911          (A) LENGTH: 648 base pairs
6912          (B) TYPE: nucleic acid
6913          (C) STRANDEDNESS: single
6914          (D) TOPOLOGY: linear
6915
6916      (ii) MOLECULE TYPE: cDNA
6917
6918
6919      (ix) FEATURE:
6920          (A) NAME/KEY: CDS
6921          (B) LOCATION: 1..648
6922
6923
--> 6924      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
6925
6926  ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
6927  Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
6928      1                      5                      10                      15
6929
6930  CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:12

INPUT SET: S30248.raw

6931	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
6932	20 25 30	
6933		
6934	TCT GGT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
6935	Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
6936	35 40 45	
6937		
6938	GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
6939	Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
6940	50 55 60	
6941		
6942	GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
6943	Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
6944	65 70 75 80	
6945		
6946	TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
6947	Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
6948	85 90 95	
6949		
6950	ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
6951	Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
6952	100 105 110	
6953		
6954	GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
6955	Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
6956	115 120 125	
6957		
6958	ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
6959	Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
6960	130 135 140	
6961		
6962	GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
6963	Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
6964	145 150 155 160	
6965		
6966	CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
6967	Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
6968	165 170 175	
6969		
6970	CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA	576
6971	Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	
6972	180 185 190	
6973		
6974	TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624
6975	Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser	
6976	195 200 205	
6977		
6978	ATG GAA ACT ACT ATG CGG TCT TGA	648
6979	Met Glu Thr Thr Met Arg Ser *	
6980	210 215	
6981		
6982	(i) SEQUENCE CHARACTERISTICS:	
6983	(A) LENGTH: 2007 base pairs	

(2) INFORMATION FOR SEQ ID NO:116:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:13

INPUT SET: S30248.raw

6984 (B) TYPE: nucleic acid  
6985 (C) STRANDEDNESS: single  
6986 (D) TOPOLOGY: linear  
6987

6988 (ii) MOLECULE TYPE: cDNA  
6989  
6990  
6991

6992 (ix) FEATURE:  
6993 (A) NAME/KEY: CDS  
6994 (B) LOCATION: 1..2004  
6995  
6996

--> 6997 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:  
6998

6999	ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
7000	Met His Met His His His His His His His Leu Val Pro Arg Gly Ser Ala	
7001	1 5 10 15	
7002		
7003	CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC AAG	96
7004	Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys	
7005	20 25 30	
7006		
7007	ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
7008	Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	
7009	35 40 45	
7010		
7011	CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC	192
7012	Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	
7013	50 55 60	
7014		
7015	GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC	240
7016	Gly Val Cys Trp Thr Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	
7017	65 70 75 80	
7018		
7019	GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288
7020	Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp	
7021	85 90 95	
7022		
7023	CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC	336
7024	Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys	
7025	100 105 110	
7026		
7027	ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC	384
7028	Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	
7029	115 120 125	
7030		
7031	ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC	432
7032	Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro	
7033	130 135 140	
7034		
7035	AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC	480
7036	Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys	

**INPUT SET: S30248.raw**

7037	145					150					155					160					
7038																					
7039	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG			528		
7040	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg					
7041					165					170					175						
7042																					
7043	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT			576		
7044	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr					
7045				180					185					190							
7046																					
7047	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA			624		
7048	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val					
7049			195					200					205								
7050																					
7051	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC			672		
7052	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly					
7053		210					215				220										
7054																					
7055	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG			720		
7056	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val					
7057	225					230				235						240					
7058																					
7059	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT			768		
7060	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr					
7061					245					250					255						
7062																					
7063	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG			816		
7064	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg					
7065				260				265						270							
7066																					
7067	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT			864		
7068	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe					
7069			275					280					285								
7070																					
7071	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT			912		
7072	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys					
7073		290					295					30									

**INPUT SET: S30248.raw**

7090																		
7091	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT		1152
7092	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His		
7093		370					375					380						
7094																		
7095	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA		1200
7096	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly		
7097	385					390					395					400		
7098																		
7099	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA		1248
7100	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro		
7101					405					410					415			
7102																		
7103	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC		1296
7104	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly		
7105				420					425					430				
7106																		
7107	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC		1344
7108	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr		
7109			435					440					445					
7110																		
7111	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG		1392
7112	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr		
7113		450					455					460						
7114																		
7115	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT		1440
7116	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr		
7117	465					470					475					480		
7118																		
7119	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG		1488
7120	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg		
7121				485					490						495			
7122																		
7123	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG		1536
7124	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala		
7125				500					505					510				
7126																		
7127	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG							

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:15

INPUT SET: S30248.raw

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7143  GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA      1776
7144  Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
7145              580                      585                      590
7146
7147  TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC      1824
7148  Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His
7149              595                      600                      605
7150
7151  GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC      1872
7152  Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val
7153              610                      615                      620
7154
7155  ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC      1920
7156  Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala
7157  625                      630                      635                      640
7158
7159  GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC      1968
7160  Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys
7161              645                      650                      655
7162
7163  GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC      2007
7164  Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
7165              660                      665

```

(2) INFORMATION FOR SEQ ID NO:11

```

7167      (i) SEQUENCE CHARACTERISTICS:
7168          (A) LENGTH: 2007 base pairs
7169          (B) TYPE: nucleic acid
7170          (C) STRANDEDNESS: single
7171          (D) TOPOLOGY: linear
7172

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7173      (ii) MOLECULE TYPE: cDNA
7174
7175
7176
7177

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7178      (ix) FEATURE:
7179          (A) NAME/KEY: CDS
7180          (B) LOCATION: 1..2004
7181
7182

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--> 7183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

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7184
7185  ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG      48
7186  Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala
7187      1                      5                      10                      15
7188
7189  CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC      96
7190  Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile
7191              20                      25                      30
7192
7193  AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT      144
7194  Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
7195              35                      40                      45

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**INPUT SET: S30248.raw**

7196																		
7197	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC		192
7198	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn		
7199		50					55					60						
7200																		
7201	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC		240
7202	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala		
7203	65					70					75					80		
7204																		
7205	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC		288
7206	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp		
7207					85					90					95			
7208																		
7209	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC		336
7210	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys		
7211				100					105					110				
7212																		
7213	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC		384
7214	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val		
7215			115					120					125					
7216																		
7217	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC		432
7218	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro		
7219		130					135					140						
7220																		
7221	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC		480
7222	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys		
7223	145					150					155					160		
7224																		
7225	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG		528
7226	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg		
7227					165					170					175			
7228																		
7229	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT		576
7230	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr		
7231				180					185					190				
7232																		
7233	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA		624
7234	Thr																	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:17

INPUT SET: S30248.raw

7249	ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG	816
7250	Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg	
7251	260 265 270	
7252		
7253	ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT	864
7254	Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe	
7255	275 280 285	
7256		
7257	CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT	912
7258	Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys	
7259	290 295 300	
7260		
7261	GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA	960
7262	Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr	
7263	305 310 315 320	
7264		
7265	GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC	1008
7266	Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala	
7267	325 330 335	
7268		
7269	ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG	1056
7270	Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu	
7271	340 345 350	
7272		
7273	GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC	1104
7274	Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala	
7275	355 360 365	
7276		
7277	ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT	1152
7278	Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His	
7279	370 375 380	
7280		
7281	TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA	1200
7282	Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly	
7283	385 390 395 400	
7284		
7285	ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA	1248
7286	Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro	
7287	405 410 415	
7288		
7289	ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC	1296
7290	Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly	
7291	420 425 430	
7292		
7293	TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC	1344
7294	Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr	
7295	435 440 445	
7296		
7297	CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG	1392
7298	Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr	
7299	450 455 460	
7300		
7301	ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT	1440

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:17

INPUT SET: S30248.raw

7302	Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr	
7303	465 470 475 480	
7304		
7305	GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG	1488
7306	Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg	
7307	485 490 495	
7308		
7309	CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG	1536
7310	Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala	
7311	500 505 510	
7312		
7313	GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG	1584
7314	Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu	
7315	515 520 525	
7316		
7317	CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG	1632
7318	Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	
7319	530 535 540	
7320		
7321	GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC	1680
7322	Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	
7323	545 550 555 560	
7324		
7325	TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA	1728
7326	Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val	
7327	565 570 575	
7328		
7329	GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA	1776
7330	Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
7331	580 585 590	
7332		
7333	TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC	1824
7334	Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	
7335	595 600 605	
7336		
7337	GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC	1872
7338	Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	
7339	610 615 620	
7340		
7341	ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC	1920
7342	Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
7343	625 630 635 640	
7344		
7345	GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC	1968
7346	Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys	
7347	645 650 655	
7348		
7349	GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC	2007
7350	Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg	
7351	660 665	

--> 7352 (2) INFORMATION FOR SEQ ID NO:118:  
7353

OK

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:20

INPUT SET: S30248.raw

	565	570	575	
7513				
7514				
7515	GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA			1776
7516	Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser			
7517	580	585	590	
7518				
7519	TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC			1824
7520	Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His			
7521	595	600	605	
7522				
7523	GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC			1872
7524	Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val			
7525	610	615	620	
7526				
7527	ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC			1920
7528	Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala			
7529	625	630	635	640
7530				
7531	GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC			1968
7532	Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys			
7533	645	650	655	
7534				
7535	GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC			2007
7536	Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Pro Leu Arg			
7537	660	665		

(2) INFORMATION FOR SEQ ID NO:11

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2007 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

7554	ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
7555	Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala	
7556	1 5 10 15	
7557		
7558		
7559		
7560	CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC	96
7561	Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile	
7562	20 25 30	
7563		
7564	ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
7565	Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:21

INPUT SET: S30248.raw

	35	40	45	
7566				
7567				
7568	CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC			192
7569	Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn			
7570	50	55	60	
7571				
7572	GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC			240
7573	Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala			
7574	65	70	75	80
7575				
7576	GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC			288
7577	Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp			
7578		85	90	95
7579				
7580	CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC			336
7581	Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys			
7582		100	105	110
7583				
7584	ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC			384
7585	Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val			
7586		115	120	125
7587				
7588	ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC			432
7589	Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro			
7590		130	135	140
7591				
7592	AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC			480
7593	Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys			
7594	145	150	155	160
7595				
7596	CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG			528
7597	Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg			
7598		165	170	175
7599				
7600	GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT			576
7601	Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr			
7602		180	185	190
7603				
7604	ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA			624
7605	Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val			
7606		195	200	205
7607				
7608	CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC			672
7609	Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly			
7610		210	215	220
7611				
7612	AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG			720
7613	Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val			
7614	225	230	235	240
7615				
7616	CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT			768
7617	Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr			
7618		245	250	255

**INPUT SET: S30248.raw**

7619																		
7620	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG		816
7621	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg		
7622				260					265					270				
7623																		
7624	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT		864
7625	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe		
7626			275					280					285					
7627																		
7628	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT		912
7629	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys		
7630		290					295					300						
7631																		
7632	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA		960
7633	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr		
7634	305					310					315					320		
7635																		
7636	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC		1008
7637	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala		
7638				325					330						335			
7639																		
7640	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG		1056
7641	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu		
7642				340					345					350				
7643																		
7644	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC		1104
7645	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala		
7646			355					360					365					
7647																		
7648	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT		1152
7649	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His		
7650		370					375					380						
7651																		
7652	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA		1200
7653	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly		
7654	385					390					395					400		
7655																		
7656	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC</					

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/198,723*

DATE: 12/09/98  
TIME: 16:07:22

INPUT SET: S30248.raw

7672	ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT	1440
7673	Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr	
7674	465 470 475 480	
7675		
7676	GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG	1488
7677	Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg	
7678	485 490 495	
7679		
7680	CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG	1536
7681	Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala	
7682	500 505 510	
7683		
7684	GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG	1584
7685	Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu	
7686	515 520 525	
7687		
7688	CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG	1632
7689	Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	
7690	530 535 540	
7691		
7692	GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC	1680
7693	Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	
7694	545 550 555 560	
7695		
7696	TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA	1728
7697	Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val	
7698	565 570 575	
7699		
7700	GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA	1776
7701	Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
7702	580 585 590	
7703		
7704	TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC	1824
7705	Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	
7706	595 600 605	
7707		
7708	GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC	1872
7709	Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	
7710	610 615 620	
7711		
7712	ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC	1920
7713	Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
7714	625 630 635 640	
7715		
7716	GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC	1968
7717	Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys	
7718	645 650 655	
7719		
7720	GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC	2007
7721	Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg	
7722	660 665	
7723		
7724	(i) SEQUENCE CHARACTERISTICS:	

(2) INFORMATION FOR SEQ ID NO:12

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:23

INPUT SET: S30248.raw

7725 (A) LENGTH: 2007 base pairs  
7726 (B) TYPE: nucleic acid  
7727 (C) STRANDEDNESS: single  
7728 (D) TOPOLOGY: linear

7729

7730 (ii) MOLECULE TYPE: cDNA

7731

7732

7733 (ix) FEATURE:

7734 (A) NAME/KEY: CDS

7735 (B) LOCATION: 1..2007

7736

7737

--> 7738 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

7739

7740 ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG 48

7741 Met His Met His His His His His His His Leu Val Pro Arg Gly Ser Ala

7742 1 5 10 15

7743

7744 CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC 96

7745 Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile

7746 20 25 30

7747

7748 ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT 144

7749 Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val

7750 35 40 45

7751

7752 CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC 192

7753 Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn

7754 50 55 60

7755

7756 GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC 240

7757 Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala

7758 65 70 75 80

7759

7760 GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC 288

7761 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp

7762 85 90 95

7763

7764 CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC 336

7765 Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys

7766 100 105 110

7767

7768 ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC 384

7769 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val

7770 115 120 125

7771

7772 ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC 432

7773 Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro

7774 130 135 140

7775

7776 AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC 480

7777 Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys



# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

DATE: 12/09/98  
TIME: 16:07:24

INPUT SET: S30248.raw

7778	145		150		155		160											
7779																		
7780	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG		528
7781	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg		
7782					165					170						175		
7783																		
7784	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT		576
7785	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr		
7786				180					185						190			
7787																		
7788	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA		624
7789	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val		
7790				195					200					205				
7791																		
7792	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC		672
7793	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly		
7794		210					215					220						
7795																		
7796	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCC	TAC	GCA	GCC	CAA	GGG	TAC	AAG	GTG		720
7797	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val		
7798	225					230					235					240		
7799																		
7800	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT		768
7801	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr		
7802					245					250					255			
7803																		
7804	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG		816
7805	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg		
7806				260					265					270				
7807																		
7808	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT		864
7809	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe		
7810				275				280					285					
7811																		
7812	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT		912
7813	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys		
7814		290					295					300						
7815																		
7816	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA		960
7817	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr		
7818	305					310					315					320		
7819																		
7820	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC		1008
7821	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala		
7822					325					330					335			
7823																		
7824	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG		1056
7825	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu		
7826				340					345					350				
7827																		
7828	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC		1104
7829	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala		
7830				355				360					365					

**INPUT SET: S30248.raw**

7831																		
7832	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT		1152
7833	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His		
7834		370					375					380						
7835																		
7836	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA		1200
7837	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly		
7838		385				390					395					400		
7839																		
7840	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA		1248
7841	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro		
7842					405					410					415			
7843																		
7844	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC		1296
7845	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly		
7846				420					425					430				
7847																		
7848	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC		1344
7849	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr		
7850			435					440					445					
7851																		
7852	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG		1392
7853	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr		
7854		450					455					460						
7855																		
7856	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT		1440
7857	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr		
7858		465				470					475					480		
7859																		
7860	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG		1488
7861	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg		
7862					485					490					495			
7863																		
7864	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG		1536
7865	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala		
7866				500					505					510				
7867																		
7868	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG		1584

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723

 DATE: 12/09/98  
 TIME: 16:07:25

INPUT SET: S30248.raw

7884	GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA	1776
7885	Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
7886	580 585 590	
7887		
7888	TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC	1824
7889	Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	
7890	595 600 605	
7891		
7892	GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC	1872
7893	Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	
7894	610 615 620	
7895		
7896	ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC	1920
7897	Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
7898	625 630 635 640	
7899		
7900	GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC	1968
7901	Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys	
7902	645 650 655	
7903		
7904	GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC	2007
7905	Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg Ser	
7906	660 665	

(2) INFORMATION FOR SEQ ID NO:1

09/198,723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTCGCCCGG GGATCCTCTA G

21

delete at end of file

1



**Examiner Please Note:**

This sequence listing follows the Old Rule Format but has a filing date on/after July 1, 1998.

Please determine the effective filing date of the case.

- If it is before July 1, 1998 - Applicants were correct in following the Old Rule Format -  
→→ Nothing further needs to be done.
- If it is after July 1, 1998 - Applicants should follow the New Rule Format-  
→→ Please request them to submit a new Sequence Listing (both in electronic and paper format) following the New Rule Format.